



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/680,684

DATE: 08/30/2004

TIME: 12:36:58

Input Set : N:\Crf3\RULE60\10680684.raw

Output Set: N:\CRF4\08302004\J680684.raw

```

1 <110> APPLICANT: Sprecher, Cindy A.
2     Kisiel, Walter
3     Foster, Donald C.
4 <120> TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS
5     AND
6     METHODS RELATING THERETO
7 <130> FILE REFERENCE: 93-14D3
8 <140> CURRENT APPLICATION NUMBER: US/10/680,684
9 <141> CURRENT FILING DATE: 2003-10-07
10 <150> PRIOR APPLICATION NUMBER: US/09/904,621
11 <151> PRIOR FILING DATE: 2001-07-13
12 <150> PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627
W--> 13 <151> PRIOR FILING DATE: PRIOR FILING DATE: 1999-03-09
14 <150> PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338
W--> 15 <151> PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05
16 <160> NUMBER OF SEQ ID NOS: 15
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 979
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (39)...(746)
26 <400> SEQUENCE: 1
27     ggacgccttg cccagcgggc cgcccgacc cctgcacc atg gac ccc gct cgc ccc      56
28                                     Met Asp Pro Ala Arg Pro
29                                     1           5
30     ctg ggg ctg tgc att ctg ctg ctt ttc ctg acg gag gct gca ctg ggc      104
31     Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu Thr Glu Ala Ala Leu Gly
32             10             15             20
33     gat gct gct cag gag cca aca gga aat aac gcg gag atc tgt ctc ctg      152
34     Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu
35             25             30             35
36     ccc cta gac tac gga ccc tgc cgg gcc cta ctt ctc cgt tac tac tac      200
37     Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr
38             40             45             50
39     gac agg tac acg cag agc tgc cgc cag ttc ctg tac ggg ggc tgc gag      248
40     Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu
41             55             60             65             70
42     ggc aac gcc aac aat ttc tac acc tgg gag gct tgc gac gat gct tgc      296
43     Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp Asp Ala Cys
44             75             80             85

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```

45      tgg agg ata gaa aaa gtt ccc aaa gtt tgc cgg ctg caa gtg agt gtg      344
46      Trp Arg Ile Glu Lys Val Pro Lys Val Cys Arg Leu Gln Val Ser Val
47              90                      95                      100
48      gac gac cag tgt gag ggg tcc aca gaa aag tat ttc ttt aat cta agt      392
49      Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys Tyr Phe Phe Asn Leu Ser
50              105                      110                      115
51      tcc atg aca tgt gaa aaa ttc ttt tcc ggt ggg tgt cac cgg aac cgg      440
52      Ser Met Thr Cys Glu Lys Phe Phe Ser Gly Gly Cys His Arg Asn Arg
53              120                      125                      130
54      att gag aac agg ttt cca gat gaa gct act tgt atg ggc ttc tgc gca      488
55      Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr Cys Met Gly Phe Cys Ala
56      135                      140                      145                      150
57      cca aag aaa att cca tca ttt tgc tac agt cca aaa gat gag gga ctg      536
58      Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu
59              155                      160                      165
60      tgc tct gcc aat gtg act cgc tat tat ttt aat cca aga tac aga acc      584
61      Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr
62              170                      175                      180
63      tgt gat gct ttc acc tat act ggc tgt gga ggg aat gac aat aac ttt      632
64      Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn Asn Phe
65              185                      190                      195
66      gtt agc agg gag gat tgc aaa cgt gca tgt gca aaa gct ttg aaa aag      680
67      Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys
68              200                      205                      210
69      aaa aag aag atg cca aag ctt cgc ttt gcc agt aga atc cgg aaa att      728
70      Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile
71      215                      220                      225                      230
72      cgg aag aag caa ttt taa acattcttaa tatgtcatct tgtttgtctt      776
73      Arg Lys Lys Gln Phe
74              235
75      tatggcttat ttgcctttat gggtgtatct gaagaataat atgacagcat gaggaacaa      836
76      atcattgggtg atttattcac cagtttttat taataacaagt cactttttca aaaatttgga      896
77      tttttttata tataactagc tgctattcaa atgtgagtct accattttta atttatgggt      956
78      caactgtttg tgagactgaa ttc      979
80 <210> SEQ ID NO: 2
81 <211> LENGTH: 235
82 <212> TYPE: PRT
83 <213> ORGANISM: Homo sapiens
84 <400> SEQUENCE: 2
85      Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
86      1              5              10              15
87      Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
88              20              25              30
89      Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
90              35              40              45
91      Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
92              50              55              60
93      Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
94      65              70              75              80

```

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```

95   Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys
96                               85                               90                               95
97   Arg Leu Gln Val Ser Val Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys
98                               100                              105                              110
99   Tyr Phe Phe Asn Leu Ser Ser Met Thr Cys Glu Lys Phe Phe Ser Gly
100                              115                              120                              125
101   Gly Cys His Arg Asn Arg Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr
102                              130                              135                              140
103   Cys Met Gly Phe Cys Ala Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser
104   145                               150                               155                               160
105   Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe
106                              165                              170                              175
107   Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly
108                              180                              185                              190
109   Gly Asn Asp Asn Asn Phe Val Ser Arg Glu Asp Cys Lys Arg Ala Cys
110                              195                              200                              205
111   Ala Lys Ala Leu Lys Lys Lys Lys Lys Met Pro Lys Leu Arg Phe Ala
112                              210                              215                              220
113   Ser Arg Ile Arg Lys Ile Arg Lys Lys Gln Phe
114   225                               230                               235

```

116 &lt;210&gt; SEQ ID NO: 3

117 &lt;211&gt; LENGTH: 30

118 &lt;212&gt; TYPE: DNA

119 &lt;213&gt; ORGANISM: Artificial Sequence

120 &lt;220&gt; FEATURE:

121 &lt;223&gt; OTHER INFORMATION: Oligonucleotide ZC4792

122 &lt;400&gt; SEQUENCE: 3

123 gttgttgctg ttgcctccgc agcctccgta

30

125 &lt;210&gt; SEQ ID NO: 4

126 &lt;211&gt; LENGTH: 30

127 &lt;212&gt; TYPE: DNA

128 &lt;213&gt; ORGANISM: Artificial Sequence

129 &lt;220&gt; FEATURE:

130 &lt;223&gt; OTHER INFORMATION: Oligonucleotide ZC6281

131 &lt;400&gt; SEQUENCE: 4

132 acagatctcc gcgttatttc ctgttggtc

30

134 &lt;210&gt; SEQ ID NO: 5

135 &lt;211&gt; LENGTH: 38

136 &lt;212&gt; TYPE: DNA

137 &lt;213&gt; ORGANISM: Artificial Sequence

138 &lt;220&gt; FEATURE:

139 &lt;223&gt; OTHER INFORMATION: Clone M-2161

140 &lt;400&gt; SEQUENCE: 5

141 gctgagagat tggagaagag agagatctgt ctccctgcc

38

143 &lt;210&gt; SEQ ID NO: 6

144 &lt;211&gt; LENGTH: 34

145 &lt;212&gt; TYPE: DNA

146 &lt;213&gt; ORGANISM: Artificial Sequence

147 &lt;220&gt; FEATURE:

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Input Set : N:\Crif3\RULE60\10680684.raw

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```

148 <223> OTHER INFORMATION: M-2177
149 <400> SEQUENCE: 6
150     gaaacctcta gacttatatc ctccagcaag catc 34
152 <210> SEQ ID NO: 7
153 <211> LENGTH: 235
154 <212> TYPE: DNA
155 <213> ORGANISM: Homo sapiens
156 <220> FEATURE:
157 <221> NAME/KEY: CDS
158 <222> LOCATION: (77)...(235)
159 <400> SEQUENCE: 7
160     gaattccatt caagaatagt tcaaacaaga agattacaaa ctatcaattt catacacaat 60
161     ataaacgacc aaaaga atg aag gct gtt ttc ttg gtt ttg tcc ttg atc gga 112
162             Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly
163             1             5             10
164     ttc tgc tgg gcc caa cca gtc act ggc gat gaa tca tct gtt gag att 160
165     Phe Cys Trp Ala Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile
166             15             20             25
167     ccg gaa gag tct ctg atc atc gct gaa aac acc act ttg gct aac gtc 208
168     Pro Glu Glu Ser Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val
169             30             35             40
170     gcc atg gct gag aga ttg gag aag aga 235
171     Ala Met Ala Glu Arg Leu Glu Lys Arg
172     45             50
174 <210> SEQ ID NO: 8
175 <211> LENGTH: 53
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 8
179     Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala
180     1             5             10             15
181     Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser
182             20             25             30
183     Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu
184             35             40             45
185     Arg Leu Glu Lys Arg
186     50
188 <210> SEQ ID NO: 9
189 <211> LENGTH: 17
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Nor-1478
194 <400> SEQUENCE: 9
195     gtaaaacgac ggccagt 17
197 <210> SEQ ID NO: 10
198 <211> LENGTH: 21
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence

```

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Input Set : N:\Crf3\RULE60\10680684.raw

Output Set: N:\CRF4\08302004\J680684.raw

```

201 <220> FEATURE:
202 <223> OTHER INFORMATION: NOR-2523
203 <400> SEQUENCE: 10
204      tctcttctcc aatctctcag c                                21
206 <210> SEQ ID NO: 11
207 <211> LENGTH: 35
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: M-2162
212 <400> SEQUENCE: 11
213      cttttactct agacttactt tgggtgcgcag aagcc                35
215 <210> SEQ ID NO: 12
216 <211> LENGTH: 10
217 <212> TYPE: PRT
218 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: N-terminal
221 <400> SEQUENCE: 12
222      Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
223      1              5              10
225 <210> SEQ ID NO: 13
226 <211> LENGTH: 8
227 <212> TYPE: PRT
228 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: N-terminal
231 <400> SEQUENCE: 13
232      Ala Gln Glu Pro Thr Gly Asn Asn
233      1              5
235 <210> SEQ ID NO: 14
236 <211> LENGTH: 165
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <221> NAME/KEY: variation
241 <222> LOCATION: (0)...(0)
242 <223> OTHER INFORMATION: Kunitz domain
243 <221> NAME/KEY: variation
244 <222> LOCATION: (1)...(3)
245 <223> OTHER INFORMATION: Codon-1 Wherein the nucleotide triplet 1-3
246      encodes any amino acid except cysteine.
W--> 247 <221> variation
248 <222> LOCATION: (4)...(6)
249 <223> OTHER INFORMATION: Codon-2 Wherein the nucleotide triplet 4-6
250      encodes any amino acid except cysteine.
W--> 251 <221> variation
252 <222> LOCATION: (160)...(162)
253 <223> OTHER INFORMATION: Codon-54 Wherein the nucleotide triplet 160-162

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/680,684

DATE: 08/30/2004  
TIME: 12:36:59

Input Set : N:\Crf3\RULE60\10680684.raw  
Output Set: N:\CRF4\08302004\J680684.raw

ase Note:

of n and/or Xaa have been detected in the Sequence Listing. Please review the  
uence Listing to ensure that a corresponding explanation is presented in the <220>  
<223> fields of each sequence which presents at least one n or Xaa.

#:14; N Pos. 1,2,3,4,5,6,160,161,162,163,164,165  
#:15; Xaa Pos. 1,2,54,55

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/680,684

DATE: 08/30/2004

TIME: 12:36:59

Input Set : N:\Crf3\RULE60\10680684.raw

Output Set: N:\CRF4\08302004\J680684.raw

L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:247 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14  
L:251 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14  
L:255 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14  
L:259 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14  
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0  
M:341 Repeated in SeqNo=14  
L:270 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:274 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15  
L:279 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15  
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
M:341 Repeated in SeqNo=15